

# SEQUENCE LISTING

<110> Giger, Roman J.

<120> IDENTIFICATION OF NOVEL NOGO-RECEPTORS  
AND METHODS RELATED THERETO

<130> 21108.0028U2

<140> 10/551,833

<141> 2005-10-03

<150> PCT/US04/010328

<151> 2004-04-02

<150> 60/460,849

<151> 2003-04-04

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 1

Met	Lys	Arg	Ala	Ser	Ser	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val	Leu
1				5				10						15	
Trp	Leu	Gln	Ala	Trp	Arg	Val	Ala	Thr	Pro	Cys	Pro	Gly	Ala	Cys	Val
			20					25				30			
Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Ser	Cys	Pro	Gln	Gln	Gly	Leu	
		35					40				45				
Gln	Ala	Val	Pro	Thr	Gly	Ile	Pro	Ala	Ser	Ser	Gln	Arg	Ile	Phe	Leu
		50				55				60					
His	Gly	Asn	Arg	Ile	Ser	Tyr	Val	Pro	Ala	Ala	Ser	Phe	Gln	Ser	Cys
65					70				75					80	
Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	Asn	Ala	Leu	Ala	Gly	Ile
			85					90						95	
Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Thr	Leu	Leu	Glu	Gln	Leu	Asp	Leu
			100					105					110		
Ser	Asp	Asn	Ala	Gln	Leu	Arg	Val	Val	Asp	Pro	Thr	Thr	Phe	Arg	Gly
		115					120					125			
Leu	Gly	His	Leu	His	Thr	Leu	His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu
		130				135					140				
Leu	Gly	Pro	Gly	Leu	Phe	Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr
145					150				155					160	
Leu	Gln	Asp	Asn	Asn	Leu	Gln	Ala	Leu	Pro	Asp	Asn	Thr	Phe	Arg	Asp
			165					170						175	

```

Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
      180      185      190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
      195      200      205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
      210      215      220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
      225      230      235      240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
      245      250      255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
      260      265      270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
      275      280      285
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
      290      295      300
Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Phe Gln
      305      310      315      320
Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys Cys
      325      330      335
Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro
      340      345      350
Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr
      355      360      365
Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe
      370      375      380
Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro
      385      390      395      400
Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg
      405      410      415
Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly
      420      425      430
Gln Ala Gly Ser Gly Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly
      435      440      445
Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu
      450      455      460
Val Leu Trp Thr Val Leu Gly Pro Cys
      465      470

```

&lt;210&gt; 2

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
 Synthetic Construct

&lt;400&gt; 2

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Pro Val Thr Pro Ser Cys Pro Met Leu Cys Thr Cys Tyr Ser Ser Pro
  1          5          10          15
Pro Thr Val Ser Cys Gln Ala Asn Asn Phe Ser Ser Val Pro Leu Ser
      20      25      30
Leu Pro Pro Ser Thr Gln Arg Leu Phe Leu Gln Asn Asn Leu Ile Arg
      35      40      45
Ser Leu Arg Pro Gly Thr Phe Gly Pro Asn Leu Leu Thr Leu Trp Leu
      50      55      60

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Phe	Ser	Asn	Asn	Leu	Ser	Thr	Ile	Tyr	Pro	Gly	Thr	Phe	Arg	His	Leu
65					70					75					80
Gln	Ala	Leu	Glu	Glu	Leu	Asp	Leu	Gly	Asp	Asn	Arg	His	Leu	Arg	Ser
			85						90					95	
Leu	Glu	Pro	Asp	Thr	Phe	Gln	Gly	Leu	Glu	Arg	Leu	Gln	Ser	Leu	His
			100					105					110		
Leu	Tyr	Arg	Cys	Gln	Leu	Ser	Ser	Leu	Pro	Gly	Asn	Ile	Phe	Arg	Gly
		115					120					125			
Leu	Val	Ser	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Glu	Asn	Ser	Leu	Leu	His
	130					135					140				
Leu	Gln	Asp	Asp	Leu	Phe	Ala	Asp	Leu	Ala	Asn	Leu	Ser	His	Leu	Phe
145					150					155					160
Leu	His	Gly	Asn	Arg	Leu	Arg	Leu	Leu	Thr	Glu	His	Val	Phe	Arg	Gly
			165						170					175	
Leu	Gly	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	Gly	Asn	Arg	Leu	Gln	Gly
			180					185					190		
Val	His	Arg	Ala	Ala	Phe	His	Gly	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Tyr
	195						200					205			
Leu	Phe	Asn	Asn	Ser	Leu	Ala	Ser	Leu	Pro	Gly	Glu	Ala	Leu	Ala	Asp
	210					215					220				
Leu	Pro	Ala	Leu	Glu	Phe	Leu	Arg	Leu	Asn	Ala	Asn	Pro	Trp	Ala	Cys
225					230					235					240
Asp	Cys	Arg	Ala	Arg	Pro	Leu	Trp	Ala	Trp	Phe	Gln	Arg	Ala	Arg	Val
			245						250					255	
Ser	Ser	Ser	Asp	Val	Thr	Cys	Ala	Thr	Pro	Pro	Glu	Arg	Gln	Gly	Arg
			260					265					270		
Asp	Leu	Arg	Thr	Leu	Arg	Asp	Thr	Asp	Phe	Gln	Ala	Cys	Pro		
	275						280					285			

<210> 3

<211> 420

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 3

Met	Leu	Pro	Gly	Leu	Arg	Arg	Leu	Leu	Gln	Gly	Pro	Ala	Ser	Ala	Cys
1				5					10					15	
Leu	Leu	Leu	Thr	Leu	Leu	Ala	Leu	Pro	Pro	Val	Thr	Pro	Ser	Cys	Pro
			20					25					30		
Met	Leu	Cys	Thr	Cys	Tyr	Ser	Ser	Pro	Pro	Thr	Val	Ser	Cys	Gln	Ala
		35				40						45			
Asn	Asn	Phe	Ser	Ser	Val	Pro	Leu	Ser	Leu	Pro	Pro	Ser	Thr	Gln	Arg
	50				55					60					
Leu	Phe	Leu	Gln	Asn	Asn	Leu	Ile	Arg	Ser	Leu	Arg	Pro	Gly	Thr	Phe
65					70					75					80
Gly	Pro	Asn	Leu	Leu	Thr	Leu	Trp	Leu	Phe	Ser	Asn	Asn	Leu	Ser	Thr
			85						90					95	
Ile	Tyr	Pro	Gly	Thr	Phe	Arg	His	Leu	Gln	Ala	Leu	Glu	Glu	Leu	Asp
			100					105					110		
Leu	Gly	Asp	Asn	Arg	His	Leu	Arg	Ser	Leu	Glu	Pro	Asp	Thr	Phe	Gln
		115					120					125			
Gly	Leu	Glu	Arg	Leu	Gln	Ser	Leu	His	Leu	Tyr	Arg	Cys	Gln	Leu	Ser
	130					135					140				

```

Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
145                               150                               155                               160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
                               165                               170                               175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
                               180                               185                               190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
                               195                               200                               205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
                               210                               215                               220
Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
225                               230                               235                               240
Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
                               245                               250                               255
Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
                               260                               265                               270
Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
                               275                               280                               285
Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
                               290                               295                               300
Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
305                               310                               315                               320
Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
                               325                               330                               335
Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
                               340                               345                               350
Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
                               355                               360                               365
Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr
370                               375                               380
Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val
385                               390                               395                               400
Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala
                               405                               410                               415
Pro His His Leu
                               420

```

&lt;210&gt; 4

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 4

```

Asn Gly Asn Ala Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu
1                               5                               10                               15
Trp Leu Arg Arg Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr
                               20                               25                               30
Pro Glu Leu Arg Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp
                               35                               40                               45
Phe Arg Asn Cys Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His
50                               55                               60
Thr Leu Ser Thr Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser
65                               70                               75                               80

```

21108.0028P1

His	Gly	Ala	Ser	Arg	Asp	Lys	Gly	His	Pro	His	Gly	His	Leu	Pro	Gly
				85					90					95	
Ser	Arg	Ser	Gly	Ser	Lys	Lys	Pro	Gly	Lys	Asn	Cys	Thr	Ser	His	Arg
			100					105					110		
Asn	Arg	Asn	Gln	Ile	Ser	Lys	Gly	Ser	Ala	Gly	Lys	Glu	Leu	Pro	Glu
			115				120					125			
Leu	Gln	Asp	Tyr	Ala	Pro	Asp	Tyr	Gln	His	Lys	Phe	Ser	Phe	Asp	Ile
	130					135					140				
Met	Pro	Thr	Ala	Arg	Pro	Lys	Arg	Lys	Gly	Lys	Cys	Ala	Arg	Arg	Thr
145					150					155					160
Pro	Ile	Arg	Ala	Pro	Ser	Gly	Val	Gln	Gln	Ala	Ser	Ser	Gly	Thr	
				165				170						175	

<210> 5

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 5

Met	Leu	Arg	Lys	Gly	Cys	Cys	Val	Glu	Leu	Leu	Leu	Leu	Leu	Leu	Ala
1				5				10						15	
Gly	Glu	Leu	Pro	Leu	Ser	Gly	Gly	Cys	Pro	Arg	Asp	Cys	Val	Cys	Tyr
			20					25					30		
Pro	Ser	Pro	Met	Thr	Val	Ser	Cys	Gln	Ala	His	Asn	Phe	Ala	Ala	Ile
		35				40					45				
Pro	Glu	Gly	Ile	Pro	Glu	Asp	Ser	Glu	Arg	Ile	Phe	Leu	Gln	Asn	Asn
	50					55					60				
His	Ile	Thr	Phe	Leu	Gln	Gly	His	Phe	Ser	Pro	Ala	Met	Val	Thr	
65				70				75						80	
Leu	Trp	Ile	Tyr	Ser	Asn	Asn	Ile	Thr	Phe	Ile	Ala	Pro	Asn	Thr	Phe
			85					90					95		
Glu	Gly	Phe	Val	His	Leu	Glu	Glu	Leu	Asp	Leu	Gly	Asp	Asn	Arg	Gln
			100					105					110		
Leu	Arg	Thr	Leu	Ala	Pro	Glu	Thr	Phe	Gln	Gly	Leu	Val	Lys	Leu	His
		115				120						125			
Ala	Leu	Tyr	Leu	Tyr	Lys	Cys	Gly	Leu	Ser	Ser	Leu	Pro	Ala	Gly	Ile
	130					135					140				
Phe	Gly	Gly	Leu	His	Ser	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	His
145				150					155						160
Ile	Glu	Tyr	Leu	Gln	Asp	Asp	Ile	Phe	Val	Asp	Leu	Val	Asn	Leu	Ser
			165					170					175		
His	Leu	Phe	Leu	His	Gly	Asn	Lys	Leu	Trp	Ser	Leu	Gly	Gln	Gly	Ile
		180				185							190		
Phe	Arg	Gly	Leu	Val	Asn	Leu	Asp	Arg	Leu	Leu	Leu	His	Glu	Asn	Gln
		195				200						205			
Leu	Gln	Trp	Val	His	His	Lys	Ala	Phe	His	Asp	Leu	His	Arg	Leu	Thr
	210					215					220				
Thr	Leu	Phe	Leu	Phe	Asn	Asn	Ser	Leu	Thr	Glu	Leu	Gln	Gly	Asp	Cys
225				230						235					240
Leu	Ala	Pro	Leu	Val	Ala	Leu	Glu	Phe	Leu	Arg	Leu	Asn	Gly	Asn	Ala
			245					250						255	
Trp	Asp	Cys	Gly	Cys	Arg	Ala	Arg	Ser	Leu	Trp	Glu	Trp	Leu	Arg	Arg
			260					265					270		

```

Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr Pro Glu Leu Arg
      275              280              285
Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp Phe Arg Asn Cys
      290              295              300
Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Ser Thr
305              310              315              320
Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
      325              330              335
Arg Asp Lys Gly His Pro His Gly His Leu Pro Gly Ser Arg Ser Gly
      340              345              350
Ser Lys Lys Pro Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
      355              360              365
Ile Ser Lys Gly Ser Ala Gly Lys Glu Leu Pro Glu Leu Gln Asp Tyr
      370              375              380
Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
385              390              395              400
Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
      405              410              415
Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Val Ser
      420              425              430
Leu Leu Ala Trp Ile Leu Gly Leu Val Val Ser Leu Arg
      435              440              445

```

&lt;210&gt; 6

&lt;211&gt; 2215

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 6

```

tcgcggacac ggggcgcacg gaccgaccga ctaaccgact ccctgcgggt ctgcgctgcc      60
gaggggcgcg gacacccgtt gtccagggtc aaccagccc tttccatctc gtcgtgcccc      120
gccccgtccc gtcggggccg atggctcctt cagaggcacg gagtccgggg ggcgcagggt      180
agagctccgc agccccgcta cgtagcccg gactcccggg tccttacgga gccccgcgga      240
gtccccgcgg tctgtccggc gggataaggg agcagagtgg agcgccctcc ccccccgcc      300
gccccctccc ccgatcgtcg agacaagatg ctgcccgggc tccggcgccct gctgcaaggt      360
cctgcctcag cctgcctcct gctgacactc ctggccctcc ctctgtgac cccagctgc      420
cctatgctct gcacctgcta ctctctccg ccacagtga gctgccaggc caacaacttc      480
tcctcggtgc cgctgtcctt gccaccagt acacagcgac tcttcttgca gaacaacctc      540
attcgctcac tgcggccagg aacttttggg cccaacctgc tcaccctgtg gctcttctcc      600
aacaacctct ccaccatcta ccctggcacc ttccgccatc tgcaggccct agaggaactg      660
gacctcggtg acaatcggca cctgcgctcc ctggagcctg acaccttcca gggcctggag      720
aggctgcagt cactacatct gtaccgggtg cagctcagca gtctgcctgg caacatcttc      780
cgaggcctgg tcagcctaca gtacctctac ctccaggaga acagcctgct ccacctacag      840
gatgacttgt tcgccgacct ggccaacctg agccaccttt tcctccacgg gaaccgcctg      900
cggctgctca cggagcacgt gttccgcggc ttgggcagcc tggaccggct gctgctgcac      960
gggaaccggc tgcagggcgt acaccgcga gccttccacg gtctcagccg cctcaccatc     1020
ctttacctgt tcaacaacag cctggcctcg ctgccgggag aggcgctggc tgacctgcca     1080
gcgctcgagt tcctgcggct caacgccaac ccctgggcgt gcgactgccg cgctcggccg     1140
ctctgggctt ggttccagcg cgcgcgggtg tccagctccg acgtgacctg cgccaccccg     1200
cccagacgcc agggccggga cctgcgcacg ctgcgcgaca ccgatttcca agcgtgcccc     1260
ccgcccacac ccacgcggcc gggcagccgc gccgcgggca acagctcttc caaccacctg     1320
tacggcggtg ccgaggcggg cgctccccc gcagacccat ccacgctcta ccgagacctg     1380
ccgcccaggg actcgcgggg gcgtcagggc ggggacgcgc ccactgagga cgactactgg     1440

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gggggctacg	gcggcgagga	ccagcgaggc	gagcagacgt	gtcccggggc	cgcggtgccag	1500
gcgcccgcgg	actcgcgtgg	ccccgtgctc	tgggcccggc	tgcgcacccc	tctgctctgc	1560
ctcttgctcc	tggctcccca	tcacctctga	ctgcggtgct	ccgatggaag	agaccacgtt	1620
cttcgccccg	ctccccttct	ctgccccacg	gagctgaggc	tccgaacttg	ccccttgttt	1680
gcgacccggc	ctggcacctt	ccctaggcct	cctcgctctt	tttcttcccc	tgaccaggct	1740
gcctcatattg	ccttccgggc	tgttgtgact	tatgtatggc	agcccctaag	acgggtgtata	1800
aggtggctcg	gccccattcg	ccctgattct	agacattaac	tcttctgccc	ccatcccaag	1860
gctggggcgt	gacaccccag	gcagccgttg	ctcctctctc	cggggcccca	cagtggactc	1920
ggaggggctt	tttgtccgca	gagcaccttc	caccagcaga	gcctttgaaa	gctccccctg	1980
ggagcctccc	ctcctccccc	tttggagggg	tgtctcagcg	aggcccaggc	tgccccctgga	2040
ccctgcttgt	cctgatccct	tcagcctcct	gacaccggag	aatacttttc	tcctaagtct	2100
acccaggaca	cttttttaggt	gcctggagag	atttctctct	accatggccc	ctgtgtgggtg	2160
aagataaaaag	aaattgtttg	ggggaaaaaa	tttattaaaa	aattctatta	ttttt	2215

&lt;210&gt; 7

&lt;211&gt; 1422

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 7

atgaagaggg	cgctcctccg	aggaagccgg	ctgctggcat	gggtgttatg	gctacaggcc	60
tggagggtag	caacgccctg	ccctgggtgcc	tgtgtgtgct	acaatgagcc	caaggtcaca	120
acaagctgcc	cccagcagg	cctgcaggct	gtacccactg	gcatcccagc	ctccagccag	180
agaatcttcc	tgcacggcaa	ccgaatctct	tacgtgccag	ccgccagctt	ccagtcatgc	240
cggaaatctca	ccatcctgtg	gctgcactca	aatgcgctgg	ccgggattga	tgccgcggcc	300
ttcactggtc	tgaccctcct	ggagcaacta	gatcttagtg	acaatgcaca	gctccgtgtc	360
gtggacccca	ccacgttccg	tggcctgggc	cacctgcaca	cgtgcacct	agaccgatgc	420
ggcctgcagg	agctggggcc	tggcctattc	cgtgggctgg	cagctctgca	gtacctctac	480
ctacaagaca	acaacctgca	ggcacttccc	gacaacacct	tccgagacct	gggcaacctc	540
acgcattctct	ttctgcatgg	caaccgtatc	cccagtggtc	ctgagcacgc	tttccgtggc	600
ttgcacagtc	ttgaccgtct	cctcttgcac	cagaaccatg	tggctcgtgt	gcacccacat	660
gccttccggg	accttgggccg	actcatgacc	ctctacctgt	ttgccaacaa	cctctccatg	720
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ccctgggtgt	gtgactgcag	ggcacgtccg	ctctgggcct	ggctgcagaa	gttccgaggt	840
tcctcatccg	agggtgccctg	caacctaccc	caacgcctgg	caggccgtga	tctgaagcgc	900
ctggctgcca	gtgacttaga	gggttgtgct	gtggcttcgg	ggcccttccg	tcccttcag	960
accaatcagc	tcactgatga	ggagctgctg	ggcctcccca	agtgttgcca	gccggatgct	1020
gcagacaagg	cctcagtact	ggaacccggg	aggccggcgt	ctgctggaaa	tgactcaag	1080
ggacgtgtgc	ctcccgtgta	cactccacca	ggcaatggct	caggcccacg	gcacatcaat	1140
gactctccat	ttgggacttt	gccgggctct	gcagagcccc	cactgactgc	cctgcggcct	1200
gggggttccg	agcccccg	actgccacc	acgggtcccc	gcaggaggcc	aggttgttcc	1260
agaaagaacc	gcacccgtag	ccactgccgt	ctgggccagg	caggaagtgg	gagcagtgga	1320
actggggatg	cagaaggttc	gggggccctg	cctgcacctg	cctgcagcct	tgctcctctg	1380
ggccttgcac	tggtactttg	gacagtgcct	gggcctgct	ga		1422

&lt;210&gt; 8

&lt;211&gt; 2601

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<220>  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> n = a, t, c, or g

```

<400> 8
tgcgcccgcc ggcgctttcc cggagctggg ctgtgcgtgc gagcgccctt ttgcagcagc      60
cgctgcccga gggggcgggg aagaggggac atcggttagc cggccagggg gcggcggtccc      120
ccctcaaaac cgcctgcaaa gtgtttgggg cggcagaatc aggccgccgg ctcggtggag      180
caagccactc gccccggggc tgagagagcg cacggcggtg gttggcagcg ccgcggttgc      240
tagcaggcgc cggtgccctg ggcgccngc ttgggctcac catgcccctg cgggaccggg      300
ccgcccggga caagcggatt cccggcttgc ccccgctcgc acgcgctcgg attagctgta      360
gctggcgccc agggatttga atctggacct caggagggag cgcgcctagg ccgacctcgg      420
aacggcgccc ccgcgcccaa catgcttcgc aaaggggtgt gtgtggaatt gctgctgttg      480
ctgctggctg gagagctacc tctgagtggg ggttgtcttc gagactgtgt gtgctacccc      540
tcgcccata ga ctgtcagttg ccaggcacac aactttgccc ccatccccga gggcatccca      600
gaggacagcg agcgcattct cctgcagaac aatcacatca ccttcctcca gcagggccac      660
ttcagccccg ccatggtcac cctctggatc tactccaaca acatcacttt cattgctccc      720
aacacctttg agggctttgt gcatctggag gagctagacc ttggagacaa ccggcagctt      780
cgaacgctgg caccgcagac ctccaaggc ctgggtgaagc ttcacgccct ctacctctac      840
aagtgcggac tgagctccct gcctgcgggc atctttgggt gcctgcacag cctgcagtac      900
ctctacttgc aggacaacca tattgagtac ctccaagatg acatctttgt ggacctgggtc      960
aacctcagtc acttgtttct ccatggcaac aagctatgga gcctggggcca gggcatcttc     1020
cggggcctgg tgaacctgga ccggttgctg ctgcatgaga accagctaca gtgggtccac     1080
cacaaggctt tccatgacct ccacaggcta accacctctt ttctcttcaa caatagcctc     1140
accgagctgc agggtgactg cctggcccc cttgggtggccc tggagtttct tcgcctcaat     1200
gggaatgctt gggactgtgg ctgccgggca cgggtccctgt gggaatggct gcgaaggttc     1260
cgtggctcca gctctgttgt cccctgcgcg actccagagc tgcggcaagg acaggacctg     1320
aagtcgctga gggttgagga ctcccggaac tgcactggac cagcgtctcc tcaccagatc     1380
aagtctcaca cgcttagcac ctctgacagg gctgcgccga aggagcacca tccctccac     1440
ggtgcctcca gggacaaagg ccaccacat ggccatctgc ctggctccag gtcaggttcc     1500
aagaagccag gcaagaactg caccagccac aggaaccgaa accagatctc taaggggagc     1560
gctgggaaag agcttcctga actgcaggac tatgcccccg actatcagca caagttcagc     1620
tttgacatca tgcccactgc acgacccaag aggaagggca agtgtgcccg caggaccccc     1680
atccgtgccc ccagtggggt gcagcaggcc tcctcaggca cggccctcgg ggtctcactc     1740
ctggcctgga tactgggggt ggtggtatct ctccgctgag gacccagggc accgtcacc     1800
agcactgcca cctgtccagc aaggaaacag aatcttttct tcttttctt tcttttctc     1860
taagtggaa ag atctgctggg ttccaggaaa aggctgctaa aaccttcagt ccagtgtgga     1920
cctttttggg ggattaaagc ccaacggtag agctgtagac aggaagggga gcacatctta     1980
cctggctgtc ctgaccgagc acctccggac agtattccac tcagccagtg gtcaaagggc     2040
acaccaagtg agtcgttagt ggtgtcagga catgtgcccc ttgaagaaat gggcttgccg     2100
aatcctggtc acttggaag aagggctgaa ggacctgct ggtttcggaa ggagcaggac     2160
tcagaacaag gctcaccag agtcagctgg ggcaaacagc aatctcagag cactcttggt     2220
cttgctgag atcacttagt taactggccc tgtccaatcc tatgcctccc tcagtcccta     2280
cccatgaggg taatgcctct cattcctgaa gtctcaggca gtccctggcag acttgctggg     2340
gttcaagaac caatcaccaa aggagagatc gccagaggat gacatataga actttactcg     2400
taatgagagt cacacagaag gtgcagtttt atacctatgt ccacttatat atatattctc     2460
actctgacca cacatccaca taatatatat atatatatta taaatatata aatgcacagg     2520
tcccccaacc cactccttac caaactgtat gtcttatcat gtttataaac tatacgggaa     2580
cctaaaaaaaa aaaaagtga a a                                     2601

```

<210> 9  
 <211> 445  
 <212> PRT  
 <213> Artificial Sequence





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Pro	Ser	Gly	Val	Gln	Gln	Ala	Ser	Ser	Gly	Thr	Ala	Leu	Gly	Val	Ser
			420					425					430		
Leu	Leu	Ala	Trp	Ile	Leu	Gly	Leu	Val	Val	Ser	Leu	Arg			
		435					440					445			

<210> 10

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 10

Met	Ala	Ala	Trp	Pro	Ser	Arg	Val	Gly	Ala	Trp	Arg	Pro	Gly	Ala	Gly
1				5					10					15	
Pro	Pro	Thr	Ser	Ala	Arg	Leu	Pro	Gly	Arg	Leu	Gly	Gln	Leu	Gly	Pro
			20					25					30		
Trp	Lys	Lys	Val	Gly	Cys	Cys	Val	Glu	Leu	Leu	Leu	Leu	Leu	Val	Ala
		35					40					45			
Ala	Glu	Leu	Pro	Leu	Gly	Gly	Gly	Cys	Pro	Arg	Asp	Cys	Val	Cys	Tyr
	50					55				60					
Pro	Ala	Pro	Met	Thr	Val	Ser	Cys	Gln	Ala	His	Asn	Phe	Ala	Ala	Ile
65				70					75						80
Pro	Glu	Gly	Ile	Pro	Val	Asp	Ser	Glu	Arg	Val	Phe	Leu	Gln	Asn	Asn
				85					90					95	
Arg	Ile	Gly	Leu	Leu	Gln	Pro	Gly	His	Phe	Ser	Pro	Ala	Met	Val	Thr
			100					105					110		
Leu	Trp	Ile	Tyr	Ser	Asn	Asn	Ile	Thr	Tyr	Ile	His	Pro	Ser	Thr	Phe
		115					120						125		
Glu	Gly	Phe	Val	His	Leu	Glu	Glu	Leu	Asp	Leu	Gly	Asp	Asn	Arg	Gln
	130					135					140				
Leu	Arg	Thr	Leu	Ala	Pro	Glu	Thr	Phe	Gln	Gly	Leu	Val	Lys	Leu	His
145					150					155					160
Ala	Leu	Tyr	Leu	Tyr	Lys	Cys	Gly	Leu	Ser	Ala	Leu	Pro	Ala	Gly	Val
				165					170					175	
Phe	Gly	Gly	Leu	His	Ser	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	His
			180					185					190		
Ile	Glu	Tyr	Leu	Gln	Asp	Asp	Ile	Phe	Val	Asp	Leu	Val	Asn	Leu	Ser
		195					200					205			
His	Leu	Phe	Leu	His	Gly	Asn	Lys	Leu	Trp	Ser	Leu	Gly	Pro	Gly	Thr
	210					215					220				
Phe	Arg	Gly	Leu	Val	Asn	Leu	Asp	Arg	Leu	Leu	Leu	His	Glu	Asn	Gln
225					230					235					240
Leu	Gln	Trp	Val	His	His	Lys	Ala	Phe	His	Asp	Leu	Arg	Arg	Leu	Thr
				245					250					255	
Thr	Leu	Phe	Leu	Phe	Asn	Asn	Ser	Leu	Ser	Glu	Leu	Gln	Gly	Glu	Cys
			260					265					270		
Leu	Ala	Pro	Leu	Gly	Ala	Leu	Glu	Phe	Leu	Arg	Leu	Asn	Gly	Asn	Pro
		275					280					285			
Trp	Asp	Cys	Gly	Cys	Arg	Ala	Arg	Ser	Leu	Trp	Glu	Trp	Leu	Gln	Arg
	290					295					300				
Phe	Arg	Gly	Ser	Ser	Ser	Ala	Val	Pro	Cys	Val	Ser	Pro	Gly	Leu	Arg
305					310					315					320
His	Gly	Gln	Asp	Leu	Lys	Leu	Leu	Arg	Ala	Glu	Asp	Phe	Arg	Asn	Cys
				325					330					335	

```

Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Thr Thr
      340      345      350
Thr Asp Arg Ala Ala Arg Lys Glu His His Ser Pro His Gly Pro Thr
      355      360      365
Arg Ser Lys Gly His Pro His Gly Pro Arg Pro Gly His Arg Lys Pro
      370      375      380
Gly Lys Asn Cys Thr Asn Pro Arg Asn Arg Asn Gln Ile Ser Lys Ala
      385      390      395      400
Gly Ala Gly Lys Gln Ala Pro Glu Leu Pro Asp Tyr Ala Pro Asp Tyr
      405      410      415
Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala Arg Pro Lys Arg
      420      425      430
Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala Pro Ser Gly Val
      435      440      445
Gln Gln Ala Ser Ser Ala Ser Ser Leu Gly Ala Ser Leu Leu Ala Trp
      450      455      460
Thr Leu Gly Leu Ala Val Thr Leu Arg
      465      470

```

&lt;210&gt; 11

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 11

```

Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
  1      5      10      15
Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
      20      25      30
Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
      35      40      45
Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
      50      55      60
Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
      65      70      75      80
Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
      85      90      95
Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
      100      105      110
Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
      115      120      125
Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
      130      135      140
Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
      145      150      155      160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
      165      170      175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
      180      185      190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
      195      200      205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
      210      215      220

```

Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala  
 225 230 235 240  
 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu  
 245 250 255  
 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu  
 260 265 270  
 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys  
 275 280 285  
 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp  
 290 295 300  
 Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Ser Pro Phe Arg Pro Phe  
 305 310 315 320  
 Gln Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys  
 325 330 335  
 Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg  
 340 345 350  
 Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp  
 355 360 365  
 Thr Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro  
 370 375 380  
 Phe Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg  
 385 390 395 400  
 Pro Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg  
 405 410 415  
 Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu  
 420 425 430  
 Gly Gln Ala Gly Ser Gly Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser  
 435 440 445  
 Gly Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala  
 450 455 460  
 Leu Val Leu Trp Thr Val Leu Gly Pro Cys  
 465 470

&lt;210&gt; 12

&lt;211&gt; 1425

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence:/Note =  
 Synthetic Construct

&lt;400&gt; 12

atgctgcccg	ggctccggcg	cctgctgcaa	ggtcctgcct	cagcctgcct	cctgctgaca	60
ctcctggccc	tcctctctgt	gacccccagc	tgccctatgc	tctgcacctg	ctactcctct	120
ccgcccacag	tgagctgcca	ggccaacaac	ttctcctcgg	tgccgctgtc	cttgccaccc	180
agtacacagc	gactcttctt	gcagaacaac	ctcattcgct	cactgcggcc	aggaactttt	240
gggcccaccc	tgctcaccct	gtggctcttc	tccaacaacc	tctccaccat	ctaccctggc	300
accttcgcgc	atctgcaggc	cctagaggaa	ctggacctcg	gtgacaatcg	gcacctgcgc	360
tccttgagc	ctgacacctt	ccagggcctg	gagaggctgc	agtcactaca	tctgtaccgg	420
tgccaggtca	gcagtctgcc	tggaacatc	ttccgaggcc	tggtcagcct	acagtacctc	480
tacctccagg	agaacagcct	gctccacctc	caggatgact	tgttcgccga	cctggccaac	540
ctgagccacc	ttttcctcca	cgggaaccgc	ctgcggtctg	tcacggagca	cgtgttccgc	600
ggcttgggca	gcctggaccg	gctgctgctg	cacgggaacc	ggctgcaggg	cgtacaccgc	660
gcagccttcc	acgggtctcag	ccgcctcacc	atcctttacc	tgttcaacaa	cagcctggcc	720
tcgctgccgg	gagaggcgct	ggctgacctg	ccagcgctcg	agttcctgcg	gctcaacgcc	780
aacccttggg	cgtgcgactg	ccgcgctcgg	ccgctctggg	cttggttcca	gcgcgcgcgg	840

```

gtgtccagct ccgacgtgac ctgcgccacc ccgcccagagc gccagggccg ggacctgcgc 900
acgctgcgcg acaccgattt ccaagcgtgc ccgccgccca ctagtcctt ccgtcccttc 960
cagaccaatc agctcactga tgaggagctg ctgggcctcc ccaagtgctg ccagccggat 1020
gctgcagaca aggcctcagt actggaaccc gggaggcccg cgtctgctgg aaatgcactc 1080
aagggacgtg tgcctcccgg tgacactcca ccaggcaatg gctcaggccc acggcacatc 1140
aatgactctc catttgggac tttgccgggc tctgcagagc cccactgac tgcctgcgcg 1200
cctggggggtt ccgagccccc gggactgccc accacgggtc cccgcaggag gccaggttgt 1260
tccagaaaga accgcacccg tagccactgc cgtctgggccc aggcaggaag tgggagcagt 1320
ggaactgggg atgcagaagg ttcgggggcc ctgcctgccc tggcctgcag ccttgctcct 1380
ctgggccttg cactggtact ttggaccgtg ctcggggcct gctga 1425

```

&lt;210&gt; 13

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 13

```

Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
1          5          10          15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
20          25          30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
35          40          45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
50          55          60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65          70          75          80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
85          90          95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
100         105         110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
115         120         125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
130         135         140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145         150         155         160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
165         170         175
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
180         185         190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
195         200         205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
210         215         220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
225         230         235         240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
245         250         255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
260         265         270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
275         280         285

```

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```
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
  290          295          300
Asp Leu Glu Gly Cys Ala Val Ala Thr Ser Pro Thr Arg Pro Gly Ser
 305          310          315          320
Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
          325          330          335
Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
          340          345          350
Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
          355          360          365
Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr
          370          375          380
Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val
 385          390          395          400
Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala
          405          410          415
Pro His His Leu
          420
```

<210> 14

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 14

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atgaagaggg cgctcctccgg aggaagccgg ctgctggcat ggggtgttatg gctacaggcc      60
tggagggtag caacgccctg cctgggtgcc tgtgtgtgct acaatgagcc caaggtcaca      120
acaagctgcc ccagcagggg cctgcaggct gtaccactg gcaccccagc ctccagccag      180
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag ccgccagctt ccagtcatgc      240
cggaatctca ccatcctgtg gctgcactca aatgcgctgg ccgggattga tgccgcggcc      300
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc      360
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc      420
ggcctgcagg agctggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac      480
ctacaagaca acaacctgca ggcacttccc gacaacacct tccgagacct gggcaacctc      540
acgcactctt ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc      600
ttgcacagtc ttgaccgtct cctcttgac cagaacctat tggctcgtgt gcacccacat      660
gccttcgggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg      720
ctccccgcag aggtcctagt gcccctgagg tctctgcagt acctgcgact caatgacaac      780
ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt      840
tcctcatccg aggtgccctg caacctaccc caacgcctgg caggccgtga tctgaagcgc      900
ctggctgcca gtgacttaga gggttgtgct gtggctacta gtcccacgcg gccgggcagc      960
cgcgcccgcg gcaacagctc ttccaaccac ctgtacggcg tggccgaggc gggcgctccc     1020
cccgcagacc catccacgct ctaccgagac ctgcccgcgg aggactcgcg ggggcgtcag     1080
ggcggggacg cgcccactga ggacgactac tgggggggct acggcggcga ggaccagcga     1140
ggcgagcaga cgtgtcccgg ggccgcgtgc caggcgcccc cggactcgcg tggccccgtg     1200
ctctcggccg ggctgcgcac ccctctgctc tgccctcttg tcctggctcc ccatcacctc     1260
tga                                             1263
```

<210> 15

<211> 415

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 15

Met	Leu	Arg	Lys	Gly	Cys	Cys	Val	Glu	Leu	Leu	Leu	Leu	Leu	Leu	Ala
1				5				10						15	
Gly	Glu	Leu	Pro	Leu	Ser	Gly	Gly	Cys	Pro	Arg	Asp	Cys	Val	Cys	Tyr
			20					25					30		
Pro	Ser	Pro	Met	Thr	Val	Ser	Cys	Gln	Ala	His	Asn	Phe	Ala	Ala	Ile
		35				40					45				
Pro	Glu	Gly	Ile	Pro	Glu	Asp	Ser	Glu	Arg	Ile	Phe	Leu	Gln	Asn	Asn
	50					55					60				
His	Ile	Thr	Phe	Leu	Gln	Gln	Gly	His	Phe	Ser	Pro	Ala	Met	Val	Thr
65				70					75						80
Leu	Trp	Ile	Tyr	Ser	Asn	Asn	Ile	Thr	Phe	Ile	Ala	Pro	Asn	Thr	Phe
			85					90					95		
Glu	Gly	Phe	Val	His	Leu	Glu	Glu	Leu	Asp	Leu	Gly	Asp	Asn	Arg	Gln
			100					105					110		
Leu	Arg	Thr	Leu	Ala	Pro	Glu	Thr	Phe	Gln	Gly	Leu	Val	Lys	Leu	His
		115				120						125			
Ala	Leu	Tyr	Leu	Tyr	Lys	Cys	Gly	Leu	Ser	Ser	Leu	Pro	Ala	Gly	Ile
	130				135						140				
Phe	Gly	Gly	Leu	His	Ser	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	His
145				150					155						160
Ile	Glu	Tyr	Leu	Gln	Asp	Asp	Ile	Phe	Val	Asp	Leu	Val	Asn	Leu	Ser
			165					170					175		
His	Leu	Phe	Leu	His	Gly	Asn	Lys	Leu	Trp	Ser	Leu	Gly	Gln	Gly	Ile
		180				185						190			
Phe	Arg	Gly	Leu	Val	Asn	Leu	Asp	Arg	Leu	Leu	Leu	His	Glu	Asn	Gln
	195				200							205			
Leu	Gln	Trp	Val	His	His	Lys	Ala	Phe	His	Asp	Leu	His	Arg	Leu	Thr
	210				215						220				
Thr	Leu	Phe	Leu	Phe	Asn	Asn	Ser	Leu	Thr	Glu	Leu	Gln	Gly	Asp	Cys
225				230					235						240
Leu	Ala	Pro	Leu	Val	Ala	Leu	Glu	Phe	Leu	Arg	Leu	Asn	Gly	Asn	Ala
			245					250					255		
Trp	Asp	Cys	Gly	Cys	Arg	Ala	Arg	Ser	Leu	Trp	Glu	Trp	Leu	Arg	Arg
		260						265				270			
Phe	Arg	Gly	Ser	Ser	Ser	Val	Val	Pro	Cys	Ala	Thr	Pro	Glu	Leu	Arg
	275					280						285			
Gln	Gly	Gln	Asp	Leu	Lys	Ser	Leu	Arg	Val	Glu	Asp	Phe	Arg	Asn	Cys
	290				295					300					
Thr	Gly	Pro	Thr	Ser	Pro	Thr	Arg	Pro	Gly	Ser	Arg	Ala	Arg	Gly	Asn
305				310					315						320
Ser	Ser	Ser	Asn	His	Leu	Tyr	Gly	Val	Ala	Glu	Ala	Gly	Ala	Pro	Pro
			325					330					335		
Ala	Asp	Pro	Ser	Thr	Leu	Tyr	Arg	Asp	Leu	Pro	Ala	Glu	Asp	Ser	Arg
		340						345				350			
Gly	Arg	Gln	Gly	Gly	Asp	Ala	Pro	Thr	Glu	Asp	Asp	Tyr	Trp	Gly	Gly
		355				360						365			
Tyr	Gly	Gly	Glu	Asp	Gln	Arg	Gly	Glu	Gln	Thr	Cys	Pro	Gly	Ala	Ala
	370				375						380				
Cys	Gln	Ala	Pro	Ala	Asp	Ser	Arg	Gly	Pro	Val	Leu	Ser	Ala	Gly	Leu
385				390					395						400
Arg	Thr	Pro	Leu	Leu	Cys	Leu	Leu	Leu	Leu	Ala	Pro	His	His	Leu	
			405					410					415		

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<210> 16

<211> 1245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 16

atgcttcgca	aagggtgctg	tgtggaattg	ctgctgttgc	tgctggctgg	agagctacct	60
ctgagtgggtg	gttgtcctcg	ctgtgtgtgc	tacctctcg	ccatgactgt	cagttgccag	120
gcacacaact	ttgccgccat	ccccgagggc	atcccagagg	acagcgagcg	catcttcctg	180
cagaacaatc	acatcacctt	cctccagcag	ggccacttca	gccccgccat	ggtcaccctc	240
tggatctact	ccaacaacat	cactttcatt	gctcccaaca	cctttgaggg	ctttgtgcat	300
ctggaggagc	tagaccttgg	agacaaccgg	cagcttcgaa	cgctggcacc	cgagaccttc	360
caaggccttg	tgaagcttca	cgccctctac	ctctacaagt	gcggactgag	ctccctgcct	420
gcgggcatct	ttggtggcct	gcacagcctg	cagtacctct	acttgcagga	caaccatatt	480
gagtacctcc	aagatgacat	ctttgtggac	ctggtcaacc	tcagtcaact	gtttctccat	540
ggcaacaagc	tatggagcct	gggccagggc	atcttcgggg	gcctggtgaa	cctggaccgg	600
ttgctgtctg	atgagaacca	gctacagtgg	gtccaccaca	aggctttcca	tgacctccac	660
aggctaacca	ccctctttct	cttcaacaat	agcctcaccg	agctgcaggg	tgactgcctg	720
gcccccttgg	tggccctgga	gtttcttcgc	ctcaatggga	atgcttgggg	ctgtggctgc	780
cgggcacggt	ccctgtggga	atggctgcga	aggttccgtg	gctccagctc	tgttgtcccc	840
tgcgcgactc	cagagctgcg	gcaaggacag	gacctgaagt	cgctgagggt	tgaggacttc	900
cggaactgca	ctggaccaac	tagtcccacg	cggccggggc	gccgcgcccg	cggcaacagc	960
tcttccaacc	acctgtacgg	cgtggccgag	gcgggcgctc	ccccgcaga	cccatccacg	1020
ctctaccgag	acctgccccg	cgaggactcg	cgggggcgctc	agggcgggga	cgcgcccact	1080
gaggacgact	actggggggg	ctacggcggc	gaggaccagc	gaggcgagca	gacgtgtccc	1140
ggggccgcgt	gccaggcgcc	cgcggactcg	cgtggccccg	tgctctcggc	cgggctgcgc	1200
acccctctgc	tctgcctctt	gctcctggct	ccccatcacc	tctga		1245

<210> 17

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 17

Met	Leu	Pro	Gly	Leu	Arg	Arg	Leu	Leu	Gln	Gly	Pro	Ala	Ser	Ala	Cys
1				5					10					15	
Leu	Leu	Leu	Thr	Leu	Leu	Ala	Leu	Pro	Pro	Val	Thr	Pro	Ser	Cys	Pro
			20					25					30		
Met	Leu	Cys	Thr	Cys	Tyr	Ser	Ser	Pro	Pro	Thr	Val	Ser	Cys	Gln	Ala
		35					40					45			
Asn	Asn	Phe	Ser	Ser	Val	Pro	Leu	Ser	Leu	Pro	Pro	Ser	Thr	Gln	Arg
		50				55					60				
Leu	Phe	Leu	Gln	Asn	Asn	Leu	Ile	Arg	Ser	Leu	Arg	Pro	Gly	Thr	Phe
65					70					75				80	
Gly	Pro	Asn	Leu	Leu	Thr	Leu	Trp	Leu	Phe	Ser	Asn	Asn	Leu	Ser	Thr
				85					90					95	
Ile	Tyr	Pro	Gly	Thr	Phe	Arg	His	Leu	Gln	Ala	Leu	Glu	Glu	Leu	Asp
			100					105						110	



```

Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
      115      120      125
Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
      130      135      140
Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
      145      150      155      160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
      165      170      175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
      180      185      190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
      195      200      205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
      210      215      220
Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
      225      230      235      240
Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
      245      250      255
Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
      260      265      270
Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
      275      280      285
Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
      290      295      300
Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
      305      310      315      320
Arg Ala Arg Gly Asn Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
      325      330      335
Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
      340      345      350
Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
      355      360      365
Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
      370      375      380
Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
      385      390      395      400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
      405      410      415
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
      420      425      430
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
      435      440      445
Leu Gly Pro Cys
      450

```

&lt;210&gt; 18

&lt;211&gt; 1359

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
 Synthetic Construct

&lt;400&gt; 18

```

atgctgcccc ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca
ctcctggccc tccctcctgt gacccccagc tgcctatgc tctgcacctg ctactcctct

```

60

120

```

ccgcccacag tgagctgcca ggccaacaac ttctcctcgg tgccgctgtc cttgccaccc 180
agtacacagc gactcttctt gcagaacaac ctcattcgct cactgcggcc aggaactttt 240
gggcccacac tgctcacctt gtggctcttc tccaacaacc tctccaccat ctacctgggc 300
accttccgcc atctgcaggc cctagaggaa ctggacctcg gtgacaatcg gcacctgcgc 360
tccctggagc ctgacacctt ccagggcctg gagaggctgc agtcactaca tctgtaccgg 420
tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagcct acagtacctc 480
tacctccagg agaacagcct gctccaccta caggatgact tggtcgccga cctggccaac 540
ctgagccacc ttttcttcca cgggaaccgc ctgcggtctg tcacggagca cgtgttccgc 600
ggcttgggca gcctggaccg gctgctgctg cacgggaacc ggctgcaggg cgtacaccgc 660
gcagccttcc acggtctcag ccgcctcacc atcctttacc tgttcaacaa cagcctggcc 720
tcgctgccgg gagaggcgct ggctgacctg ccagcgctcg agttcctgcg gctcaacgcc 780
aaccctggg cgtgcgactg ccgcgctcgg ccgctctggg cttggttcca gcgcgcgcgg 840
gtgtccagct ccgacgtgac ctgcgccacc ccgcccagc gccagggccg ggacctgcgc 900
acgctgcgcg acaccgattt ccaagcgtgc ccgcccacca caccacgcg gccgggcgcg 960
cgcgcccgcg gcaacactag tcccgggagg ccggcgctctg ctggaaatgc actcaaggga 1020
cgtgtgcctc ccggtgacac tccaccaggc aatggctcag gcccacggca catcaatgac 1080
tctccatttg ggactttgcc gggctctgca gagccccac tgactgccct gcggcctggg 1140
ggttccgagc ccccgggact gccaccacg ggtccccgca ggaggccagg ttgttccaga 1200
aagaaccgca ccgtagcca ctgccgtctg ggccaggcag gaagtgggag cagtggaaact 1260
ggggatgcag aaggttcggg ggccctgcct gccctggcct gcagccttgc tcctctgggc 1320
cttgcaactg tactttggac cgtgctcggg cctgctga 1359

```

&lt;210&gt; 19

&lt;211&gt; 441

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 19

```

Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1           5           10          15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
          20          25          30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
          35          40          45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
          50          55          60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65          70          75          80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
          85          90          95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
          100         105         110
Ser Asp Asn Ala Gln Leu Arg Val Asp Pro Thr Thr Phe Arg Gly
          115         120         125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
          130         135         140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145         150         155         160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
          165         170         175
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
          180         185         190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu

```

195	200	205
Leu His Gln Asn His Val	Ala Arg Val His Pro	His Ala Phe Arg Asp
210	215	220
Leu Gly Arg Leu Met Thr	Leu Tyr Leu Phe Ala	Asn Asn Leu Ser Met
225	230	235
Leu Pro Ala Glu Val Leu	Val Pro Leu Arg Ser	Leu Gln Tyr Leu Arg
245	250	255
Leu Asn Asp Asn Pro Trp	Val Cys Asp Cys Arg	Ala Arg Pro Leu Trp
260	265	270
Ala Trp Leu Gln Lys Phe	Arg Gly Ser Ser Ser	Glu Val Pro Cys Asn
275	280	285
Leu Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys	Arg Leu Ala Ala Ser
290	295	300
Asp Leu Glu Gly Cys Ala	Val Ala Ser Gly Pro	Phe Arg Pro Phe Gln
305	310	315
Thr Asn Gln Leu Thr Asp	Glu Glu Leu Leu Gly	Leu Pro Lys Cys Cys
325	330	335
Gln Pro Asp Ala Ala Asp	Lys Ala Ser Val Thr	Ser Ser Asn His Leu
340	345	350
Tyr Gly Val Ala Glu Ala	Gly Ala Pro Pro Ala	Asp Pro Ser Thr Leu
355	360	365
Tyr Arg Asp Leu Pro Ala	Glu Asp Ser Arg Gly	Arg Gln Gly Gly Asp
370	375	380
Ala Pro Thr Glu Asp Asp	Tyr Trp Gly Gly Tyr	Gly Gly Glu Asp Gln
385	390	395
Arg Gly Glu Gln Thr Cys	Pro Gly Ala Ala Cys	Gln Ala Pro Ala Asp
405	410	415
Ser Arg Gly Pro Val Leu	Ser Ala Gly Leu Arg	Thr Pro Leu Leu Cys
420	425	430
Leu Leu Leu Leu Ala Pro	His His Leu	
435	440	

&lt;210&gt; 20

&lt;211&gt; 1326

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 20

atgaagaggg	cgctcctccg	aggaagccgg	ctgctggcat	gggtgttatg	gctacaggcc	60
tggagggtag	caacgccctg	ccctgggtgc	tgtgtgtgct	acaatgagcc	caaggtcaca	120
acaagctgcc	cccagcagg	cctgcaggct	gtacccactg	gcatcccagc	ctccagccag	180
agaatcttcc	tgcacggcaa	ccgaatctct	tacgtgccag	ccgccagctt	ccagtcatgc	240
cggaatctca	ccatcctgtg	gctgcactca	aatgcgctgg	ccgggattga	tgccgcggcc	300
ttcactggtc	tgaccctcct	ggagcaacta	gatcttagtg	acaatgcaca	gctccgtgtc	360
gtggacccca	ccacgttccg	tggcctgggc	cacctgcaca	cgctgcacct	agaccgatgc	420
ggcctgcagg	agctggggcc	tggcctattc	cgtgggctgg	cagctctgca	gtacctctac	480
ctacaagaca	acaacctgca	ggcacttccc	gacaacacct	tccgagacct	gggcaacctc	540
acgcattctt	ttctgcatgg	caaccgtatc	cccagtgttc	ctgagcacgc	tttccgtggc	600
ttgcacagtc	ttgaccgtct	cctcttgac	cagaaccatg	tggctcgtgt	gcaccacat	660
gccttccggg	accttgggcc	actcatgacc	ctctacctgt	ttgccaacaa	cctctccatg	720
ctccccgcag	aggtcctagt	gcccctgagg	tctctgcagt	acctgcgact	caatgacaac	780
ccctgggtgt	gtgactgcag	ggcacgtccg	ctctgggcct	ggctgcagaa	gttccgaggt	840
tcctcatccg	aggtgccctg	caacctaccc	caacgcctgg	caggccgtga	tctgaagcgc	900

```

ctggctgcca gtgacttaga gggttgtgct gtggttcgg ggcccttcg tcccttcag      960
accaatcagc tcaactgatga ggagctgctg ggcctcccca agtgctgcca gccggatgct    1020
gcagacaagg cctcagtaac tagttccaac cacctgtacg gcgtggccga ggcgggcgct    1080
ccccccgcag acccatccac gctctaccga gacctgcccg ccgaggactc gcgggggcgt    1140
cagggcgggg acgcgcccac tgaggacgac tactgggggg gctacggcgg cgaggaccag    1200
cgaggcgagc agacgtgtcc cggggccgcg tgccaggcgc ccgcggactc gcgtggcccc    1260
gtgctctcgg ccgggctgcg caccctctct ctctgctctt tgctcctggc tccccatcac    1320
ctctga                                1326

```

&lt;210&gt; 21

&lt;211&gt; 452

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 21

```

Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1          5          10          15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
          20          25          30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
          35          40          45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
          50          55          60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65          70          75          80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
          85          90          95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
          100          105          110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
          115          120          125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
          130          135          140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145          150          155          160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
          165          170          175
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
          180          185          190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
          195          200          205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
210          215          220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
225          230          235          240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
          245          250          255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
          260          265          270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
          275          280          285
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
290          295          300

```

```

Asp Leu Glu Gly Cys Ala Val Ala Thr Ser Pro Thr Arg Pro Gly Ser
305                      310                      315                      320
Arg Ala Arg Gly Asn Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
                      325                      330                      335
Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
                      340                      345                      350
Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
                      355                      360                      365
Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
                      370                      375                      380
Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
385                      390                      395                      400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
                      405                      410                      415
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
                      420                      425                      430
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
                      435                      440                      445
Leu Gly Pro Cys
450

```

&lt;210&gt; 22

&lt;211&gt; 1359

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 22

```

atgaagaggg cgctcctccgg aggaagccgg ctgctggcat ggggtgttatg gctacaggcc      60
tggagggtag caacgccctg ccctgggtgcc tgtgtgtgct acaatgagcc caaggtcaca      120
acaagctgcc cccagcaggg cctgcaggct gtacccactg gcatcccagc ctccagccag      180
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag ccgccagctt ccagtcatgc      240
cggaatctca ccatacctgtg gctgcactca aatgcgctgg ccgggattga tgccgcggcc      300
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gtcctgtgtc      360
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc      420
ggcctgcagg agctggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac      480
ctacaagaca acaacctgca ggcacttccc gacaacacct tccgagacct gggcaacctc      540
acgcatctct ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc      600
ttgcacagtc ttgaccgtct cctcttgca cagaaccatg tggctcgtgt gcaccacat      660
gccttccggg accttgggcc actcatgacc ctctacctgt ttgccaacaa cctctccatg      720
ctccccgcag aggtcctagt gccctgagg tctctgcagt acctgcgact caatgacaac      780
ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt      840
tcctcatccg aggtgccctg caacctaccc caacgcctgg caggccgtga tctgaagcgc      900
ctggctgcca gtgacttaga gggttgtgct gtggtacta gacccacgcg gccgggcagc      960
cgcgcccgcg gcaacactag tcccgggagg ccggcgctct ctggaaatgc actcaaggga      1020
cgtgtgcctc ccggtgacac tccaccaggc aatggctcag gcccacggca catcaatgac      1080
tctccatttg ggactttgcc gggctctgca gagcecccac tgactgccct gcggcctggg      1140
ggttccgagc ccccgggact gccaccacg ggtccccgca ggaggccagg ttgttccaga      1200
aagaaccgca cccgtagcca ctgccgtctg ggccaggcag gaagtgggag cagtgggaact      1260
ggggatgcag aaggttcggg ggccctgctt gccctggcct gcagccttgc tcctctgggc      1320
cttgactggt tactttggac cgtgctcggg ccctgctga

```

&lt;210&gt; 23

&lt;211&gt; 452

21108.0028P1

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 23

Met	Leu	Pro	Gly	Leu	Arg	Arg	Leu	Leu	Gln	Gly	Pro	Ala	Ser	Ala	Cys
1				5					10					15	
Leu	Leu	Leu	Thr	Leu	Leu	Ala	Leu	Pro	Pro	Val	Thr	Pro	Ser	Cys	Pro
			20					25					30		
Met	Leu	Cys	Thr	Cys	Tyr	Ser	Ser	Pro	Pro	Thr	Val	Ser	Cys	Gln	Ala
		35					40					45			
Asn	Asn	Phe	Ser	Ser	Val	Pro	Leu	Ser	Leu	Pro	Pro	Ser	Thr	Gln	Arg
	50					55				60					
Leu	Phe	Leu	Gln	Asn	Asn	Leu	Ile	Arg	Ser	Leu	Arg	Pro	Gly	Thr	Phe
65					70					75					80
Gly	Pro	Asn	Leu	Leu	Thr	Leu	Trp	Leu	Phe	Ser	Asn	Asn	Leu	Ser	Thr
			85						90					95	
Ile	Tyr	Pro	Gly	Thr	Phe	Arg	His	Leu	Gln	Ala	Leu	Glu	Glu	Leu	Asp
			100					105					110		
Leu	Gly	Asp	Asn	Arg	His	Leu	Arg	Ser	Leu	Glu	Pro	Asp	Thr	Phe	Gln
		115				120						125			
Gly	Leu	Glu	Arg	Leu	Gln	Ser	Leu	His	Leu	Tyr	Arg	Cys	Gln	Leu	Ser
	130					135					140				
Ser	Leu	Pro	Gly	Asn	Ile	Phe	Arg	Gly	Leu	Val	Ser	Leu	Gln	Tyr	Leu
145					150					155					160
Tyr	Leu	Gln	Glu	Asn	Ser	Leu	Leu	His	Leu	Gln	Asp	Asp	Leu	Phe	Ala
			165						170					175	
Asp	Leu	Ala	Asn	Leu	Ser	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Leu	Arg
			180					185					190		
Leu	Leu	Thr	Glu	His	Val	Phe	Arg	Gly	Leu	Gly	Ser	Leu	Asp	Arg	Leu
		195					200					205			
Leu	Leu	His	Gly	Asn	Arg	Leu	Gln	Gly	Val	His	Arg	Ala	Ala	Phe	His
	210					215					220				
Gly	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Tyr	Leu	Phe	Asn	Asn	Ser	Leu	Ala
225					230					235					240
Ser	Leu	Pro	Gly	Glu	Ala	Leu	Ala	Asp	Leu	Pro	Ala	Leu	Glu	Phe	Leu
			245						250				255		
Arg	Leu	Asn	Ala	Asn	Pro	Trp	Ala	Cys	Asp	Cys	Arg	Ala	Arg	Pro	Leu
		260						265					270		
Trp	Ala	Trp	Phe	Gln	Arg	Ala	Arg	Val	Ser	Ser	Ser	Asp	Val	Thr	Cys
		275					280					285			
Ala	Thr	Pro	Pro	Glu	Arg	Gln	Gly	Arg	Asp	Leu	Arg	Thr	Leu	Arg	Asp
	290					295					300				
Thr	Asp	Phe	Gln	Ala	Cys	Pro	Pro	Pro	Thr	Pro	Thr	Arg	Pro	Gly	Ser
305					310					315					320
Arg	Ala	Arg	Gly	Glu	Thr	Ser	Pro	Gly	Arg	Pro	Ala	Ser	Ala	Gly	Asn
			325						330					335	
Ala	Leu	Lys	Gly	Arg	Val	Pro	Pro	Gly	Asp	Thr	Pro	Pro	Gly	Asn	Gly
		340						345					350		
Ser	Gly	Pro	Arg	His	Ile	Asn	Asp	Ser	Pro	Phe	Gly	Thr	Leu	Pro	Gly
	355					360						365			
Ser	Ala	Glu	Pro	Pro	Leu	Thr	Ala	Leu	Arg	Pro	Gly	Gly	Ser	Glu	Pro
	370					375					380				
Pro	Gly	Leu	Pro	Thr	Thr	Gly	Pro	Arg	Arg	Arg	Pro	Gly	Cys	Ser	Arg

21108.0028P1

```

385          390          395          400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
          405          410          415
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
          420          425          430
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
          435          440          445
Leu Gly Pro Cys
          450
```

<210> 24

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 24

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atgctgcccc ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca      60
ctcctggccc tccctcctgt gacccccagc tgccctatgc tctgcacctg ctactcctct      120
ccgcccacag tgagctgcca ggccaacaac ttctcctcgg tgccgctgtc cttgccaccc      180
agtacacagc gactcttctt gcagaacaac ctcatctcgt cactgcggcc aggaactttt      240
gggcccacac tgctcaccct gtggtctctt tccaacaacc tctccaccat ctaccctggc      300
accttccgcc atctgcaggc cctagaggaa ctggacctcg gtgacaatcg gcacctgcgc      360
tccctggagc ctgacacctt ccagggcctg gagaggctgc agtcactaca tctgtaccgg      420
tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagcct acagtacctc      480
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ctgagccacc ttttcctcca cgggaaccgc ctgcggtctg tcacggagca cgtgttcgcg      600
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gcagccttcc acggtctcag ccgcctcacc atcctttacc tgttcaacaa cagcctggcc      720
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cgcgcccgcg ggaaactagt cccgggaggc cggcgtctgc tggaaatgca ctcaagggac     1020
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agaaccgcac ccgtagccac tgccgtctgg gccaggcagg aagtgggagc agtggaaactg     1260
gggatgcaga aggttcgggg gccctgcctg ccctggcctg cagccttgct cctctggggc     1320
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<210> 25

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 25

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Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg
  1              5              10              15
Leu
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21108.0028P1

<210> 26  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 26  
Thr Ala Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr  
1 5 10

<210> 27  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 27  
His Ser Gly Ala Gly  
1 5

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 28  
gccatcccgg agggcatccc 20

<210> 29  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 29  
acacttatag aggtagaggg cgtg 24